Abstract

There is disclosed an improved high-throughput and quantitative process for determining methylation patterns in genomic DNA samples based on amplifying modified nucleic acid, and detecting methylated nucleic acid based on amplification-dependent displacement of specifically annealed hybridization probes. Specifically, the inventive process provides for treating genomic DNA samples with sodium bisulfite to create methylation-dependent sequence differences, followed by detection with fluorescence-based quantitative PCR techniques. The process is particularly well suited for the rapid analysis of a large number of nucleic acid samples, such as those from collections of tumor tissues